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SEQUENCE LISTING

<110> Reinherz, Ellis L. Freund, Christian Li, Jing Nishizawa, Kazuhisa Wagner, Gerhard <120> Cloning and Characterization of a CD2 Binding Protein (CD2BP2) <130> 1062.1021-004 <150> US 60/111,007 <151> 1998-12-04 <150> US 60/115,647 <151> 1999-01-13 <150> PCT/US99/26993 <151> 1999-11-15 <160> 25 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 1299 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (121)...(1143) <400> 1 agtectette egggtgatgg eggegggtge eeeggatgta geeetggege aageatetet 60 tettttttee acctegeett eegeggatte ceagettgag aaacacetet ttgeecegte 120 atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag 168 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp gag gat gaa atc att gtc ccc aag aag aag ctg gtg gac cct gtg gct 216 Glu Asp Glu Ile Ile Val Pro Lys Lys Leu Val Asp Pro Val Ala ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp age gat gag gag gat gat gat gat ggg ggg tee age aaa tat gae 312 Ser Asp Glu Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc 360

Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro

70

agc Ser	gag Glu	gly aaa	ggt Gly	ggt Gly 85	cgg Arg	atc Ile	aca Thr	ccc Pro	ttt Phe 90	aac Asn	ctg Leu	cag Gln	gag Glu	gag Glu 95	atg Met	408
gag Glu	gaa Glu	ggc Gly	cac His 100	ttt Phe	gat Asp	gcc Ala	gat Asp	ggc Gly 105	aac Asn	tac Tyr	ttc Phe	ctg Leu	aac Asn 110	cgg Arg	gat Asp	456
gct Ala	cag Gln	atc Ile 115	cga Arg	gac Asp	agc Ser	tgg Trp	ctg Leu 120	gac Asp	aac Asn	att Ile	gac Asp	tgg Trp 125	gtg Val	aag Lys	atc Ile	504
cgg Arg	gag Glu 130	cgg Arg	cca Pro	cct Pro	ggc Gly	cag Gln 135	cgc Arg	cag Gln	gcc Ala	tca Ser	gac Asp 140	tcg Ser	gag Glu	gag Glu	gag Glu	552
			ggc Gly													600
ctt Leu	ttg Leu	gag Glu	ctc Leu	cta Leu 165	ttg Leu	cct Pro	aga Arg	gag Glu	aca Thr 170	gtg Val	gct Ala	gly aaa	gca Ala	ctg Leu 175	agg Arg	648
cgt Arg	ctg Leu	gly ggg	gcc Ala 180	cga Arg	gga Gly	gga Gly	ggc Gly	aaa Lys 185	Gly 999	aga Arg	aag Lys	glà aaa	cct Pro 190	Gly 999	caa Gln	696
ccc Pro	agt Ser	tcc Ser 195	cct Pro	cag Gln	cgc Arg	ctg Leu	gac Asp 200	cgg Arg	ctc Leu	tcc Ser	Gly	ttg Leu 205	gcc Ala	gac Asp	cag Gln	744
atg Met	gtg Val 210	gcc Ala	cgg Arg	ggc Gly	aac Asn	ctt Leu 215	ggt Gly	gtg Val	tac Tyr	cag Gln	gaa Glu 220	aca Thr	agg Arg	gaa Glu	cgg Arg	792
ttg Leu 225	gct Ala	atg Met	cgt Arg	ctg Leu	aag Lys 230	ggt Gly	ttg Leu	ggg Gly	tgt Cys	cag Gln 235	acc Thr	cta Leu	gga Gly	ccc Pro	cac His 240	840
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tcg Ser	cgg Arg	gga Gly 275	gat Asp	ggt Gly	ctg Leu	gtg Val	gat Asp 280	gtg Val	atg Met	tgg Trp	gaa Glu	tat Tyr 285	aag Lys	tgg Trp	gag Glu	984
aac Asn	acg Thr 290	Gly aaa	gat Asp	gcc Ala	gag Glu	ctg Leu 295	tat Tyr	Gly aaa	ccc Pro	ttc Phe	acc Thr 300	agc Ser	gcc Ala	cag Gln	atg Met	1032

cag Glr 305	acc Thr	tgg Trp	gtg Val	agt Ser	gaa Glu 310	Gly	tac Tyr	ttc Phe	ccg Pro	gac Asp 315	Gly	gtt Val	tat Tyr	tgc Cys	cgg Arg 320	1080
aag Lys	ctg Leu	gac Asp	ccc Pro	cct Pro 325	ggt Gly	ggt Gly	cag Gln	ttc Phe	tac Tyr 330	aac Asn	tcc Ser	aaa Lys	cgc Arg	att Ile 335	gac Asp	1128
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Glu	Asp	Glu	Ile 20	Ile	Val	Pro	Lys		Lys	Leu	Val	Asp			Ala	
Gly	Ser	Gly 35		Pro	Gly	Ser	Arg	25 Phe	Lys	Gly	Lys	His	30 Ser	Leu	Asp	
Ser	Asp 50		Glu	Glu	Asp	Asp 55		Asp	Gly	Gly	Ser 60		Lys	Tyr	Asp	
	Leu	Ala	Ser	Glu		Val	Glu	Gly	Gln			Ala	Thr	Leu		
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Glu	Glu	Gly			Asp	Ala	Asp			Tyr	Phe	Leu	Asn		Asp	
Ala	Gln		100 Arg	Asp	Ser	Trp		105 Asp	Asn	Ile	Asp		110 Val	Lys	Ile	
Arg	Glu	115 Arg	Pro	Pro	Gly	Gln	120 Arg	Gln	Ala	Ser	Asp	125 Ser	Glu	Glu	Glu	
Asp	130 Ser	Leu	Glv	Gln	Thr	135 Ser	Met	Ser	Δla	Gln	140 Ala	T. 11	T.211	Gl 11	Glv	
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Leu	Leu	GIu	Leu	Leu 165	Leu	Pro	Arg	Glu	Thr 170	Val	Ala	Gly	Ala	Leu 175	Arg	
Arg	Leu	Gly	Ala 180	Arg	Gly	Gly	Gly	Lys 185	Gly	Arg	Lys	Gly	Pro 190		Gln	
Pro	Ser	Ser 195		Gln	Arg	Leu	Asp		Leu	Ser	Gly	Leu 205		Asp	Gln	
Met	Val 210		Arg	Gly	Asn	Leu 215		Val	Tyr	Gln	Glu 220		Arg	Glu	Arg	
Leu 225	Ala	Met	Arg	Leu			Leu	Gly	Cys			Leu	Gly	Pro		
	Pro	Thr	Pro		230 Pro	Ser	Leu	Asp	Met	235 Phe	Ala	Glu	Glu	Leu	240 Ala	
Glu	Glu	Glu		245 Glu	Thr	Pro	Thr		250 Thr	Gln	Arg	Gly	Glu	255 Ala	Glu	
Ser	Arg	Gly	260 Asp	Gly	Leu	Val	Asp	265 Val	Met	Trp	Glu	Tyr	270 Lys	Trp	Glu	
	Thr	275				Leu	280				Thr	285				
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Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
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Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
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Phe Asp Leu Tyr Thr
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Phe
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Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro
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Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser
Leu Ser Pro Ser Ser Asn
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Pro Phe Thr Ile Gln Met Met Ser Gln Trp Tyr Ile Gly Gly Tyr Phe
Ala Ser Thr
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Thr Pro Thr
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Pro Pro Gly His Arg
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